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Minimum
Maximum
                                                                                                                                                                     Database :
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                             DB DB
                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
                                                                                     PIR_66:*
1: pir1:*
2: pir2:*
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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375
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001, 15:52:38 ; Search time 170.72 Seconds (without alignments) 26.250 Million cell updates/sec
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SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	IJ	4	ω	2	₩.	Result No.	•
71	71	71	71	71	71.5	71.5	72	72	73.5	74	74	74.5	75	75.5	76	76	77	78	78	79	81	84.5	84.5	95	116.5	120	121	129	Score	
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T18267	T08588	A39248	B54024	136911	A45973	T25169	A53234	œ	O,		T01662			A46419	A57783	T29475	I36930	A48686	T15132	S71628	D82493	Т13998	T44430	S35221	S22477	S06398	FWCNAB	S08059	ID	
multidrug resistan		recept	protein kinase (EC	involucrin L - dou	trichohyalin – hum	۳		vicilin-like stora	ŗį	ia)	ma	profilaggrin – rat	. involucrin S - dou	trophoblast-endoth			involucrin - white	probable RNA helic	ATP-dependent RNA	sensory transducti	erved hypot	۲	n PV100	lin		tу	-globulin B	alpha-globulin typ	Description	

A; Reference number: S06398

ALIGNMENTS

alpha-globulin B precursor (clone C72) - upland cotton N,Alternate names: seed storage protein; vicilin precursor C:Species: Gossyplum hirsutum (upland cotton) C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999 C:Accession: A30838; S06911
R;Chlan, C.A.: Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A.Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N.Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: SO8059 A;Molocule type: mRNA A;Residues: 1-588 <CHL> A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375 A;Experimental source: var. Coker 201 A;Experimental source: var. Coker 201 A;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 Plant Mol. Biol. 9, 533-546, 1987 A;Title: Developmental blochemistry of cottonseed embryogenesis and germination. A; Molecule type: DNA A; Residues: 1-509 <CHL> C; Superfamily: glycinin R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987
R;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. A;Reference number: S06598
R;Accession: S08059 B Qy В Qy A; Reference number: A30838 A; Accession: A30838 A; Status: not compared with conceptual translation Matches Query Match Best Local Similarity 46 ------NPQRG------GSGRYEEGEEKQSDNP 66 60 KQQCVRECREKYQENPWRGEREEEAEEEETEEGEQEQSHNP 100 1 DPQRR-YEECQQECRQQEERQQPQCQQRCLKRFEQEQQQSQRQFQECQQHCHQQEQRPEK 59 3 DPQQREYEDCRRHCEQQEPRLQYQCQRRC-----QEQQ-------RQHGRGGDLM---- 45 36; Conservative 34.4%; 9; Score 129; DB 2; Pred. No. 3.6e-06; Mismatches 18; Length 509; Indels 38; Gaps <u>ن</u>

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R;McHenry, L.; Fritz, P.J.

Plant Mol. Biol. 18, 1173-1176, 1992

A;Title: Comparison of the structure and nucleotide sequence
A;Reference number: S22477; MUID:92288309

A;Accession: S22477
                                                                                                                                                                                                  C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: S22477; S22478; S18105; S22050
                                                                                                                                                                                                                                                                                   RESULT
S22477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted
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A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.
                                                            A; Molecule type: DNA
A; Residues: 1-566 <MCH>
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C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
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C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
A; Molecule type: mRNA
                    A; Accession: S22478
                                         A; Cross-references: EMBL: X62625
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A; Residues: 1-605 < CHL>
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A; Accession: S06398
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Best Local
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31.4%;
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Pred. No. 2.8e-05;
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Pred. No. 3.6e-05;
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A; Residues: J-452 <MC2>
A; Cross references: EMBL: X62626
C; Genetics:
A; Introns: 211/1; 269/3; 296/3; 391/3; 50
C; Superfamily: 91ycinin
C; Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status pr
F;25-566/Product: vicilin #status predict
                                                                     R:Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M. J. Biol. Chem. 274, 2563-2570, 1999
A:Title: Multiple functional proteins are produced A; Reference number: 222767; MUID:99107919
A:Accession: T44430
                                                                                                                                                                protein PV100 [imported] - winter squash C;Species: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence_revision 21-J.C;Accession: T44430
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C:Superfamily: glycinin
C:Keywords: glycoprotein
E:174-190/Product: globulin Begl #status predicted
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062
                    A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-810 <YAM>
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A; Residues: 1-637 <HEC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision
C;Accession: S35221
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A;Cross-references: GB:AE004357;
A;Experimental source: serogroup
C;Genetics:
A;Gene: VCA0171
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                               R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein VCA0171 [imported] - Vibrio cholerae (group O1 C;Species: Vibrio cholerae (group O1 C;Species: Vibrio cholerae (C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene mastermind protein - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: T13998
R;Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Evol. 38, 637-641, 1994
A;Title: Drive-selection equilibrium: homopolymer evolution in t
A;Reference number: 217850; MUID:94365848
A;Accession: T13998
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                                                           Qy
                                                                                                                                                                                                                                                                                                 A; Title: DNA Sequence of both chromosomes of A; Reference number: A82035; MUID: 20406833 A; Accession: D82493
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A; Residues: 1-646 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1655 <NEW>
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                             KRDPQQREYEDCKRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEE 60
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                                                                                                                                                                                                                   GB:AE003853; NID:g9657547; Ol; strain N16961; biotype
                                                                                                         Score 81;
Pred. No.
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No. 0.23;
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T15132
                                                                            C; Genetics:
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C;Function: modulates cell response to change A;Description: modulates cell response to change C;Superfamily: response regulator homology C;Keywords: phosphoprotein; signal transduction F;1520-1629/Domain: response regulator homology F;1568/Binding site: phosphate (Asp) (covalent)
A:Gene: CESP:glh-1
A:Map position: 1
C:Superfamily: unassigned DEAD/H box helicases;
                                                                                                                A:Cross-references: EMBL:AF000197; NID:g1947004; PID:g1947009; PIDN:AAB52901.1; GSPDB A;Experimental source: strain Bristol N2; clone T21G5
                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-604 <MIN>
                                                                                                                                                                                                                   A; Status: preliminary; translated
                                                                                                                                                                                                                                                  A; Reference number: Z18299
A; Accession: T15132
                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosm
                                                                                                                                                                                                                                                                                                                                                                                    ATP-dependent RNA helicase GLH-1 - Caenorhabditis elegans (fragment) C:Species: Caenorhabditis elegans C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 26-MC:Date: 20-Sep-1999 #text_change 26-MC:Accession: T15132
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A;Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYWY',238-1671 <SCW>
A;Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1;
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A; Accession: $78068
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R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
submitted to the EMBL Data Library, March 1996
A;Description: The hybrid histidine kinase DokA is part of the osmotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Molecule type: DNA
A:Residues: 1-1670 <SCH>
A;Cross-references: EMBL:X96869
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R;Schuster, S.C.; Noegel, A
EMBO J. 15, 3880-3889, 1996
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 29-Oct-1999
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Pred. No. 1.6;
L8; Mismatches
                                                                                                                                                                                                                         from GB/EMBL/DDBJ
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     DEAD/H box helicase
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C; Keywords: cornified cell envelope;
F; 153-386/Region: 10-residue repeats
                                                                                               A;Introns: #status absent C;Superfamily: involucrin
                                                                                                                                                                        A;Cross-references: GB:M67478; NID:g176629; PIDN:AAA35405.1; PID:g176630 C;Comment: During the terminal differentiation of keratinocytes, this protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Roussell, D.L.; Bennett, K.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 9300-9304, 1993
A;Title: glh-1, a germ-line putative RNA helicase from Caenorhabditis, has four zinc
A;Reference number: A48686; MUID:94022363
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A48686
                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                        A;Title: The involucrin genes of the white-fronted capuchin and cottontop tamarin: The A;Reference number: A57783; MUID:92114750
A;Accession: I36930
                                                                                                                                                                                                                                                                                                              R; Phillips, M.A.; Rice, R.H.; Djian, P.; Green, Mol. Biol. Evol. 8, 579-591, 1991
                                                                                                                                                                                                                                                                                                                                                 involucrin - white-fronted capuchin
C;Species: Cebus albifrons (white-fronted capuchin, pale-fronted
C;Date: 16-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 2
C;Accession: 136930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: unassigned DEAD/H box helicases;
C;Keywords: ATP; P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-707 < ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable RNA helicase glh-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
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                                                                                                                                                           linked envelope under the plasma
                                                                                                                                                                                                                    A; Residues: 1-428 < RES>
                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A48686
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   Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 GNDGFGGDGGFGGGEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 MNPQRGGSGRYEEGEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 MNPQRGGSGRYEEGEEK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RDPQQREYEDCRRHCEQQEPRLQYQCQ-----RRCQEQQRQH------GRGGDL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQPGHRS-SDCPEPRKEREPRVCYNCQQPGHTSRECTEERKPREGRTGGFGGGAGFGNNG 63
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                                                                                                                                                           membrane
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   Score
                                                         duplication; epidermis; tandem repeat
(Q-E-G-Q-[PLV]-[KE]-[LH]-[PL]-E-Q)
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   77;
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22-Jun-1999
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Query Match
Best Local
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C;Superfamily: involucrin
C;Keywords: cornified cell envelope;
F;152-451/Region: 10-residue repeats
                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-493 <RES>
A;Residues: 1-493 <RES>
A;Cross-references: GB:M67477; NID:g343313; PIDN:AAA36950.1; PID:g343314
C;Comment: During the terminal differentiation of keratinocytes, this protein from
                                                                                                                                                                                                                                                                                                                                                                            involucrin - cotton-top tamarin

(;Speciles: Saguinus oedipus (cotton-top tamarin)

C;Date: 16-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 22-Jun-1999

C;Accession: A57783

R;Phillips, M.A.; Rice, R.H.; Djian, P.; Green, H.

Mol. Biol. Evol. 8, 579-591, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:ACCESSAUM, H.; Wohldmann, P.
R:Bradshaw, H.; Wohldmann, P.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                A; Title: The involucrin genes of the white-fronted A; Reference number: A57783; MUID:92114750 A; Accession: A57783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: The sequence A; Reference number: 220623 A; Accession: T29475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T01D1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
                                                                                                A; Introns: #status absent
                                                                                                                             C; Genetics:
                                                                                                                                                       linked envelope under the plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 2
A; Introns: 25/3; 304/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U80455; PIDN:AAB37887.1; GSPDB:GN00020; CESP:T01D1.6 A;Experimental source: strain Bristol N2; clone T01D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-411 <BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 GRSEYNTAPPQQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 QQQCQQDCQAACPQQQQP--QQQCQQQCQTTCQSDDQYSQQLIQQQTYAQPGQI--PAYT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 HLEQEEKQLEHP 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 GSGRYEEGEEKQ
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29.2%;
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Pred. No. 0.97;
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7; Mismatches
     duplication; epidermis; tandem repeat
(Q-E-G-Q-[PLV]-[KE]-[LH]-{PL}-E-Q)
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Similarity

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Score Pred.

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DB 1.1;

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Length 493

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A;Cross-references: GB:M99578; NID:g187241; PIDN:AAA36187.1; PID:g187242
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:117872, NCBIP:117873)
R;E1l1son, J.W.; Ramos, C.; Yen, P.H.; Shapiro, L.J.
Hum. Mol. Genet. 1, 691-696, 1992
A;Title: Structure and expression of the human pseudoautosomal gene XE7.
A;Reference number: 154325; MUID:93258310
A;Recession: 168598
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rrophoblast-endothelial-activated lymphocyte surface protein 721P - human N;Alternate names; gene XE7 protein C;Species: Homo sapiens (man) C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Accession: A46419; I68598 R;Voland, J.R.; Myzykowski, R.J.; Huang, M.; Dutton, R.W. Proc. Natl. Acad. Sci. U.S.A. 89, 10425-10429, 1992 A;Title: Cloning and sequencing of a trophoblast-endothelial-activated lymphocyte surface A;Reference number: A46419; MUID:93066251
                                                                                                                                                       δÃ
                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mrNA
A;Residues: 1-384,'L' <RES>
A;Cross-references: GB:L03426; NID:g340386; PIDN:AAA61303.1; PID:g340387
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Search completed: March
Job time: 563 sec
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A; Introns: 254/3; 304/2; 384/3
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A; Residues: 1-550 < VOL>
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                     470 PADRVVRLCERHHAAPPRGPAPGRCPQGEPG-PPRGRRRSQKRERERGRGG----PMQGG 524
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Pred. No. 1
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